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ENTERED   PCT10

RAW SEQUENCE LISTING   DATE: 07/17/2002
PATENT APPLICATION: US/10/048,116   TIME: 09:33:37

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\07172002\J048116.raw**

```
      3 <110> APPLICANT: C.N.R.S.
      5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED FROM
THESE PROTEINS,
      6        ANALOGOUS TO MOLECULES INVOLVED IN IMMUNE RESPONSES
      8 <130> FILE REFERENCE: CP/BB 1181
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/048,116
C--> 11 <141> CURRENT FILING DATE: 2002-05-24
     13 <160> NUMBER OF SEQ ID NOS: 2
     15 <170> SOFTWARE: PatentIn Ver. 2.1
     17 <210> SEQ ID NO: 1
     18 <211> LENGTH: 1484
     19 <212> TYPE: DNA
     20 <213> ORGANISM: Artificial sequence
     22 <220> FEATURE:
     23 <221> NAME/KEY: CDS
     24 <222> LOCATION: (1)..(1482)
     26 <220> FEATURE:
     27 <223> OTHER INFORMATION: Description of Artificial Sequence: ligation
     28        fragments of DNA
     30 <400> SEQUENCE: 1
     31 atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc    48
     32 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
     33  1               5                  10                  15
     35 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta.   96
     36 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
     37                 20                  25                  30
     39 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag   144
     40 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
     41             35                  40                  45
     43 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat   192
     44 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
     45        50                  55                  60
     47 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc   240
     48 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
     49  65                 70                  75                  80
     51 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac   288
     52 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
     53                 85                  90                  95
     55 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag   336
     56 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
     57                 100                 105                 110
     59 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag   384
     60 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
     61             115                 120                 125
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63  ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc     432
64  Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
65      130             135             140
67  aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat     480
68  Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
69  145             150             155             160
71  gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct     528
72  Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
73              165             170             175
75  tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg     576
76  Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
77              180             185             190
79  gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag     624
80  Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
81          195             200             205
83  att cca gcc ccc atg tca gag ctg aca gaa act gga ggt gga gga tcc     672
84  Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser
85      210             215             220
87  act aca gct cca tca gct cag ctc gaa aaa gag ctc cag gcc ctg gag     720
88  Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
89  225             230             235             240
91  aag gaa aat gca cag ctg gaa tgg gag ttg caa gca ctg gaa aag gaa     768
92  Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
93              245             250             255
95  ctg gct cag gca gca tct gag ccc aga ggg ccc aca atc aag ccc tgt     816
96  Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
97              260             265             270
99  cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc     864
100 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
101         275             280             285
103 ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc ctg agc     912
104 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
105     290             295             300
107 ccc ata gtc aca tgt gtg gtg gtg gat gtg agc gag gat gac cca gat     960
108 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
109 305             310             315             320
111 gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca gct cag    1008
112 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
113             325             330             335
115 aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg gtc agt    1056
116 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
117             340             345             350
119 gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag ttc aaa    1104
120 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
121         355             360             365
123 tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga acc atc    1152
124 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
125     370             375             380
127 tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc ttg cct    1200
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RAW SEQUENCE LISTING   DATE: 07/17/2002
PATENT APPLICATION: US/10/048,116   TIME: 09:33:37

Input Set : A:\EP.txt
Output Set: N:\CRF3\07172002\J048116.raw

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128 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
129 385                 390                 395                 400
131 cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg   1248
132 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
133                 405                 410                 415
135 gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac   1296
136 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
137                 420                 425                 430
139 ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct   1344
140 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
141             435                 440                 445
143 gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac   1392
144 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
145         450                 455                 460
147 tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg   1440
148 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
149 465                 470                 475                 480
151 cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt aa        1484
152 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
153                 485                 490
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 921
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: Description of artificial sequence: Ligation
164       fragments of DNA
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(921)
170 <400> SEQUENCE: 2
171 atg gct ctg cag atc ccc agc ctc ctc ctc tca gct gct gtg gtg gtg   48
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173 1               5                   10                  15
175 ctg atg gtg ctg agc agc ccc ggg act gag ggc gga aac tcc atc tgc   96
176 Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly Gly Asn Ser Ile Cys
177             20                  25                  30
179 ttc tcg ccg tcg ctg gag cac ccg atc gtg gtg tcc ggc agc tgg gac   144
180 Phe Ser Pro Ser Leu Glu His Pro Ile Val Val Ser Gly Ser Trp Asp
181         35                  40                  45
183 gga ggt ggg ggc tca cta gtg ccc cga ggc tct gga ggt gga ggc tcc   192
184 Gly Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Gly Ser
185     50                  55                  60
187 gaa agg cat ttc gtg gtc cag ttc aag ggc gag tgc tac tac acc aac   240
188 Glu Arg His Phe Val Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn
189 65                  70                  75                  80
191 ggg acg cag cgc ata cgg ctc gtg acc aga tac atc tac aac cgg gag   288
192 Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu
193                 85                  90                  95
```

```
195 gag tac gtg cgc tac gac agc gac gtg ggc gag tac cgc gcg gtg acc   336
196 Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
197         100             105             110
199 gag ctg ggg cgg cca gac gcc gag tac tgg aac agc cag ccg gag atc   384
200 Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile
201         115             120             125
203 ctg gag cga acg cgg gcc gag gtg gac acg gcg tgc aga cac aac tac   432
204 Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr
205     130             135             140
207 gag ggg ccg gag acc agc acc tcc ctg cgg cgg ctt gaa cag ccc aat   480
208 Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn
209 145             150             155             160
211 gtc gcc atc tcc ctg tcc agg aca gag gcc ctc aac cac cac aac act   528
212 Val Ala Ile Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr
213             165             170             175
215 ctg gtc tgt tcg gtg aca gat ttc tac cca gcc aag atc aaa gtg cgc   576
216 Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg
217             180             185             190
219 tgg ttc agg aat ggc cag gag gag aca gtg ggg gtc tca tcc aca cag   624
220 Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln
221         195             200             205
223 ctt att agg aat ggg gac tgg acc ttc cag gtc ctg gtc atg ctg gag   672
224 Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu
225     210             215             220
227 atg acc cct cat cag gga gag gtc tac acc tgc cat gtg gag cat ccc   720
228 Met Thr Pro His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro
229 225             230             235             240
231 agc ctg aag agc ccc atc act gtg gag tgg agg gca cag tcc gag tct   768
232 Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser
233             245             250             255
235 gcc cgg agc aag gga ggt gga gga tcc act aca gct cca tca gct cag   816
236 Ala Arg Ser Lys Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln
237         260             265             270
239 ttg aaa aag aaa ttg caa gca ctg aag aaa aag aac gct cag ctg aag   864
240 Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys
241     275             280             285
243 tgg aaa ctt caa gcc ctc aag aag aaa ctc gcc cag cat cat cat cat   912
244 Trp Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln His His His His
245     290             295             300
247 cat cat tga                                                        921
248 His His
249 305
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/17/2002
PATENT APPLICATION: US/10/048,116   TIME: 09:33:38

Input Set : A:\EP.txt
Output Set: N:\CRF3\07172002\J048116.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY   DATE: 07/17/2002
PATENT APPLICATION: **US/10/048,116**   TIME: 09:33:38

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\07172002\J048116.raw**

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date